

In the Specification

Please amend the paragraph at page 20, lines 16-23 as follows:

In a preferred embodiment, recombinant ammonia producing cells are stable and produce high levels of urease in the absence of exogenous nickel. Preferably, integration vectors include, but are not limited to the mannitol operon of *S. mutans* UA159 which is targeted as the insertion sight. (The target gene cluster is annotated as smuO82 in the Oral Pathogens database (~~http://www.stlgen-lant.gov/oragen/~~). Mannitol is only poorly cariogenic and in most cases is not a major constituent of the human diet. It is rather poorly metabolized by *S. mutans*[[,]]; therefore, loss of mannitol utilization capabilities does not affect competitive fitness of the organism *in vivo*.

Please amend the paragraph beginning on page 24, line 13 through page 25, line 3 as follows:

Sequence similarity searches can be performed manually or by using several available computer programs known to those skilled in the art. Preferably, Blast and Smith-Waterman algorithms, which are available and known to those skilled in the art, and the like can be used. Blast is NCBI's sequence similarity search tool designed to support analysis of nucleotide and protein sequence databases. Blast can be accessed through the world wide web of the Internet, ~~at, for example, ncbi.nlm.nih.gov/BLAST/~~. The GCG Package provides a local version of Blast that can be used either with public domain databases or with any locally available searchable database. GCG Package v9.0 is a commercially available software package that contains over 100 interrelated software programs that enables analysis of sequences by editing, mapping, comparing and aligning them. Other programs included in the GCG Package include, for example, programs which facilitate RNA secondary structure predictions, nucleic acid fragment assembly, and evolutionary analysis. In addition, the most prominent genetic databases (GenBank, EMBL, PIR, and SWISS-PROT) are distributed along with the GCG Package and are fully accessible with the database searching and manipulation programs. GCG can be accessed through the Internet ~~at, for example, http://www.gcg-~~

~~com/~~. Fetch is a tool available in GCG that can get annotated GenBank records based on accession numbers and is similar to Entrez. Another sequence similarity search can be performed with GeneWorld and GeneThesaurus from Pangea. GeneWorld 2.5 is an automated, flexible, high-throughput application for analysis of polynucleotide and protein sequences. GeneWorld allows for automatic analysis and annotations of sequences. Like GCG, GeneWorld incorporates several tools for homology searching, gene finding, multiple sequence alignment, secondary structure prediction, and motif identification. GeneThesaurus 1.0 is a sequence and annotation data subscription service providing information from multiple sources, providing a relational data model for public and local data.

Please amend the paragraph at page 56, lines 15-24 as follows:

Construction of alkali-generating plaque streptococci: Development of stable, ammonia-producing plaque streptococci has been achieved with the design and engineering of new strains that produce high levels of urease in the absence of exogenous nickel. We have engineered new integration vectors for use in *Streptococcus* *mutans*. In this case, the mannitol operon of *S. mutans* UA159 was targeted as the insertion sight. See for example, figures 12A-12D and figure 13. Mannitol is only poorly cariogenic and in most cases is not a major constituent of the human diet. It is rather poorly metabolized by *S. mutans*, so loss of mannitol utilization capabilities should not affect competitive fitness of the organism in vivo. The target gene cluster is annotated as smu1082 in the Oral Pathogens database (~~<http://www.stdgen.lanl.gov/oragen/>~~).